FIG. 1

Minimal & Optimal Growth Temeratures for Selected Strains of Bacillus coagulans

Legend:
- ATCC #31284 GYE
- GBI-01 GYE
- GBI-01 TSA
- GBI-20 GYE
- GBI-20 TSA
- GBI-30 TSA
- ATCC #31284 TSA

FIG. 2

ATCC 3128 (1% ISOLATE)

OD 590nm

Strain + Water TSB TSB + O2
NB NB + O2 GYEB
GYEB + O2 BUGM BUGM + O2

FIG.3

OD 590nm

0.2, 0.18, 0.16, 0.14, 0.12, 0.1, 0.08, 0.06, 0.04, 0.02, 0

0.185
0.12
0.011
0.069
0.086
0.041

ATCC 3128 (99% ISOLATE)

■ Strain + Water   ■ TSB   □ TSB + O2
■ NB   □ NB + O2   ■ GYEB
□ GYEB + O2   □ BUGM   □ BUGM + O2

FIG. 4

OD 590nm

0.7 0.6 0.5 0.4 0.3 0.2 0.1 0

20DEG. STR. 30DEG. STR.

■ STRAIN + WATER   ■ STRAIN + TSB+O2
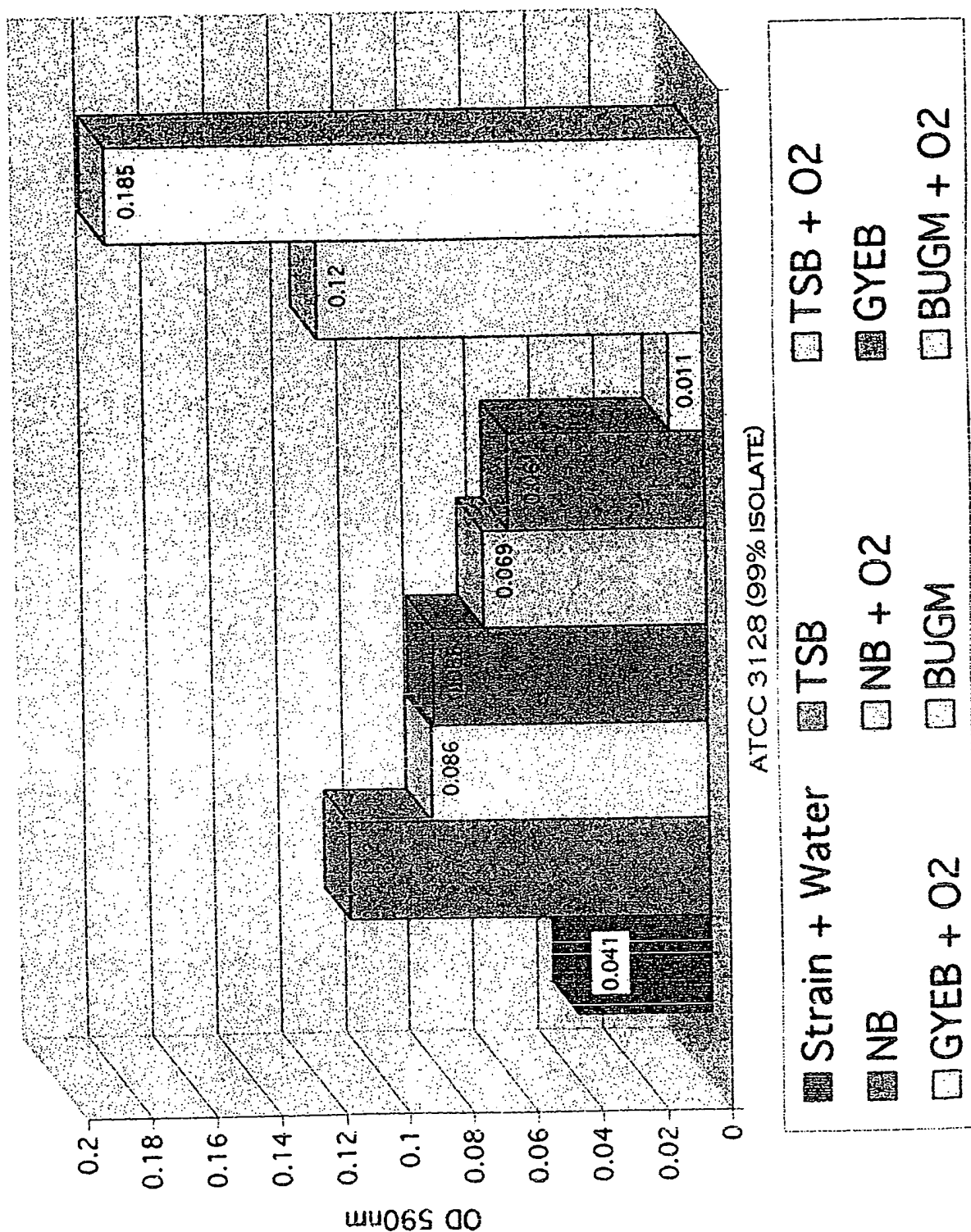□ STRAIN + TSB   ■ STRAIN + GYEB+O2
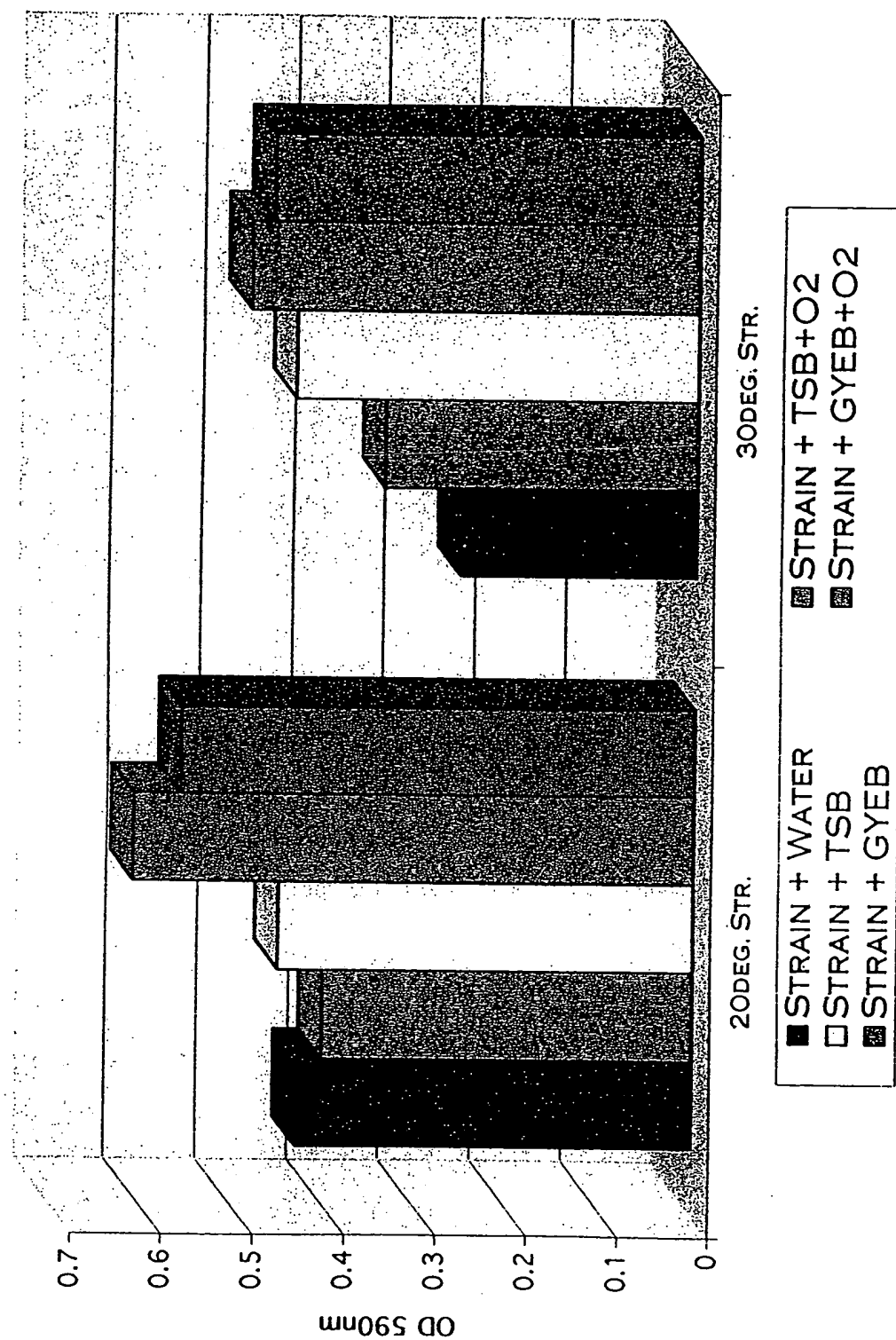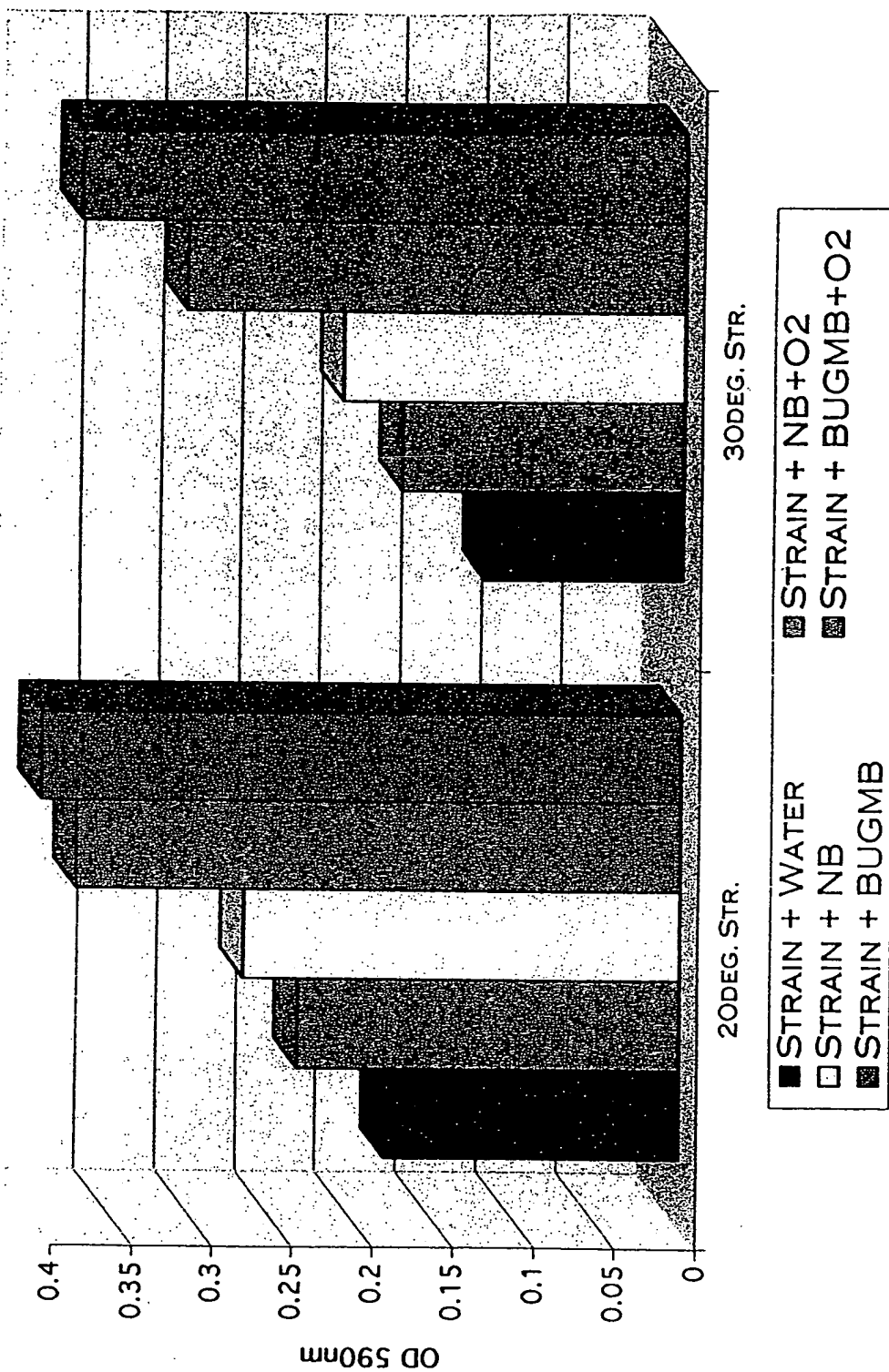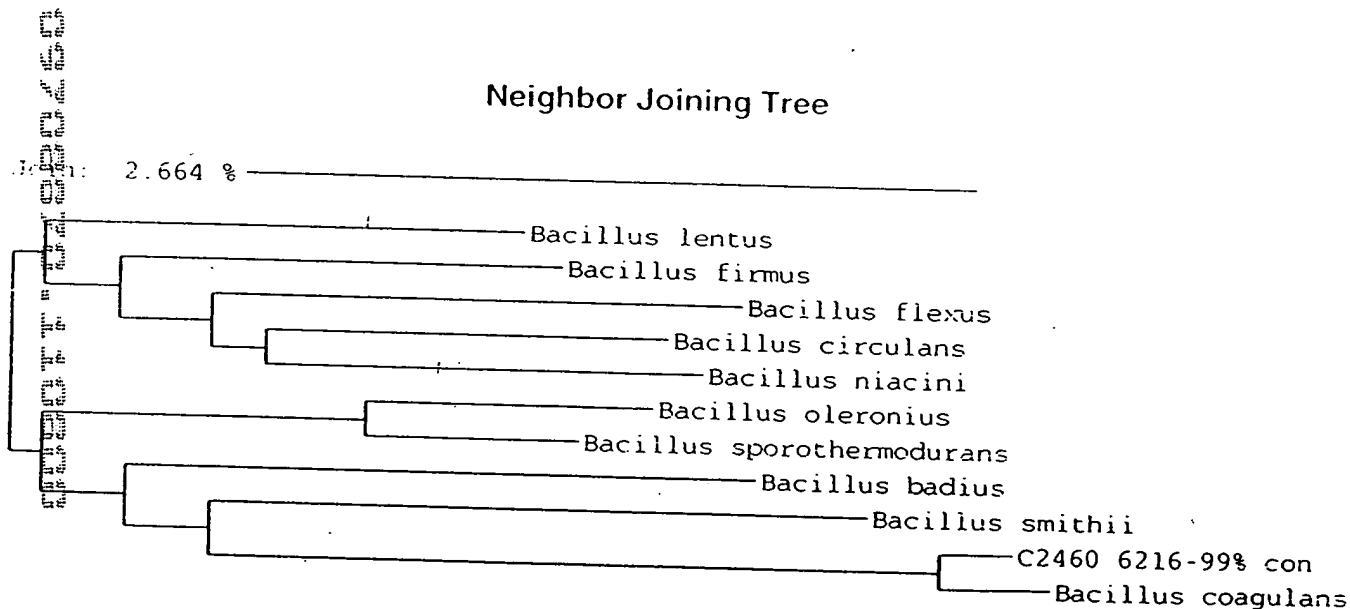■ STRAIN + GYEB

FIG. 5

FIG. 6

Alignment: 1549 C2460 6216-99% con
```
0..65 % 1549 Bacillus coagulans
4.84 % 1548 Bacillus oleronius
5.36 % 1550 Bacillus smithii
5.62 % 1548 Bacillus sporothermodurans
5.65 % 1551 Bacillus badius
5.79 % 1547 Bacillus firmus
5.85 % 1547 Bacillus lentus
5.90 % 1543 Bacillus circulans
5.95 % 1545 Bacillus niacini
6.30 % 1548 Bacillus flexus
```

Neighbor Joining Tree

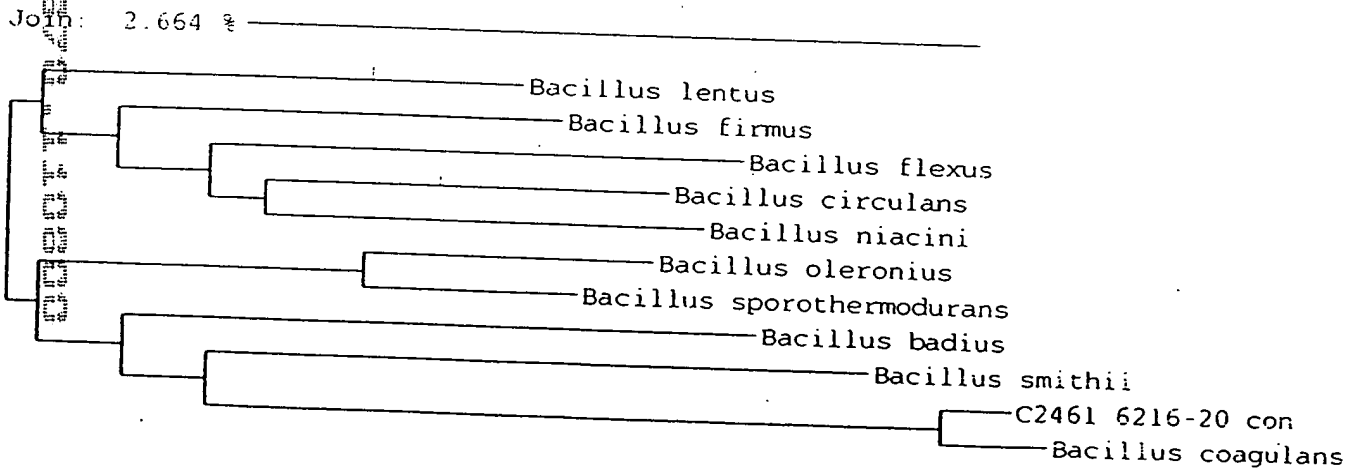Concise Alignment

```
             1
     111222222241
     347011256784
     902967240204
```
C2460 6216-99% con TCGAYTTWTTYC (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCG (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)

FIG. 7

```
Alignment:  1549 C2461 6216-20 con
 0.65 %  1549 Bacillus coagulans
 4.84 %  1548 Bacillus oleronius
 5.36 %  1550 Bacillus smithii
 5.62 %  1548 Bacillus sporothermodurans
 5.65 %  1551 Bacillus badius
 5.79 %  1547 Bacillus firmus
 5.85 %  1547 Bacillus lentus
 5.90 %  1543 Bacillus circulans
 5.95 %  1545 Bacillus niacini
 6.30 %  1548 Bacillus flexus
```

Neighbor Joining Tree

Join: 2.664 %

Concise Alignment
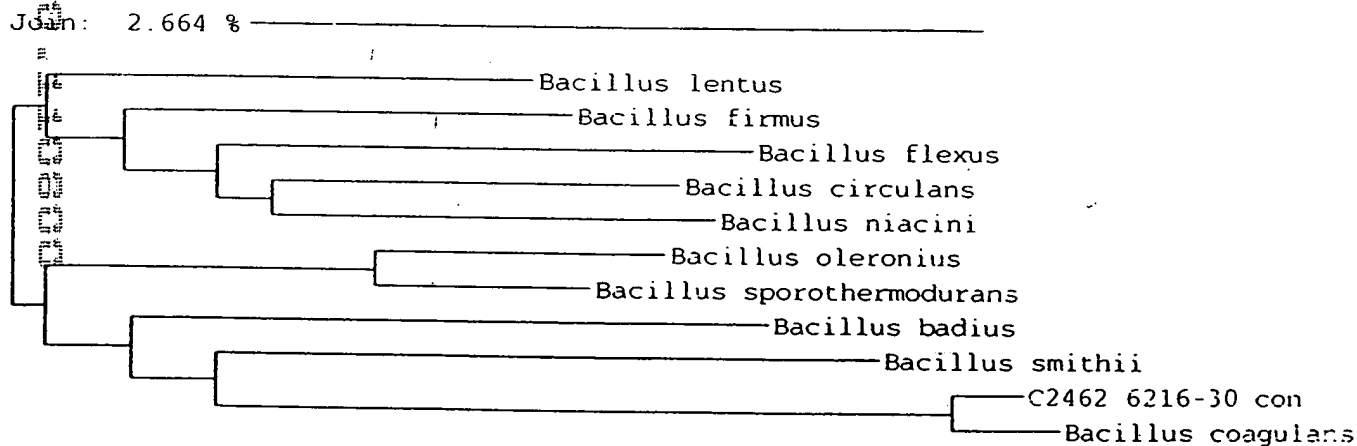
```
                         1
              111222222241
              347011256784
              902967240204
C2461 6216-20 con  TCGAYTTWTTYC    (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCG    (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)
```

FIG. 8

```
Alignment:   1549 C2462 6216-30 con
  0.65 %  1549 Bacillus coagulans
  4.84 %  1548 Bacillus oleronius
  5.36 %  1550 Bacillus smithii
  5.62 %  1548 Bacillus sporothermodurans
  5.65 %  1551 Bacillus badius
  5.79 %  1547 Bacillus firmus
  5.85 %  1547 Bacillus lentus
  5.90 %  1543 Bacillus circulans
  5.95 %  1545 Bacillus niacini
  6.30 %  1549 Bacillus flexus
```

Neighbor Joining Tree

```
Join:  2.664 %
                                    Bacillus lentus
                                    Bacillus firmus
                                    Bacillus flexus
                                    Bacillus circulans
                                    Bacillus niacini
                                    Bacillus oleronius
                                    Bacillus sporothermodurans
                                    Bacillus badius
                                    Bacillus smithii
                                    C2462 6216-30 con
                                    Bacillus coagulans
```

Concise Alignment

```
                      1
               111222222241
               347011256784
               902967240204
C2462 6216-30 con  TCGAYTTWTTYC (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCCCACCCG (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)
```
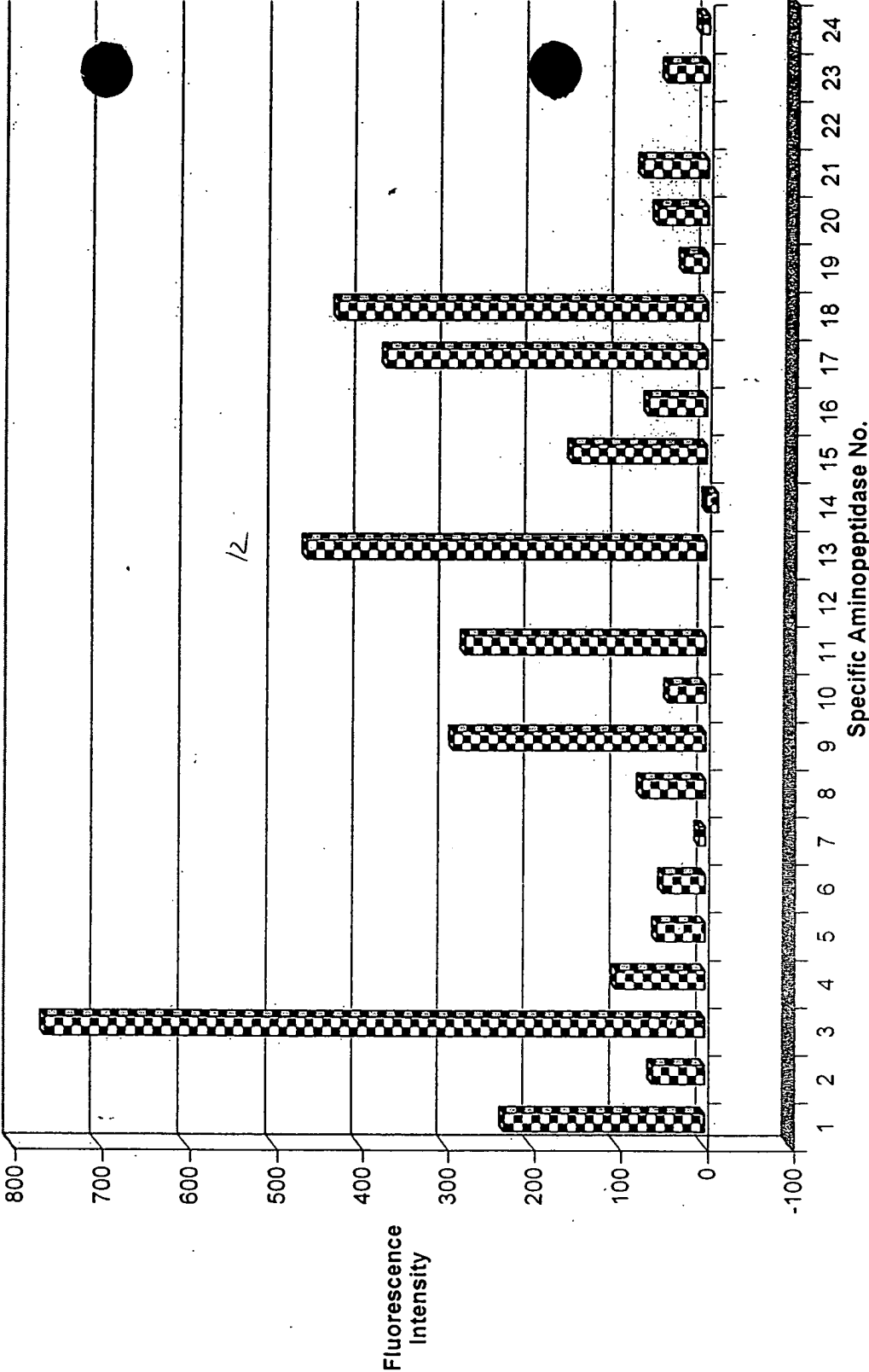
Plate #1 Bacillus 99% ATCC Isolate
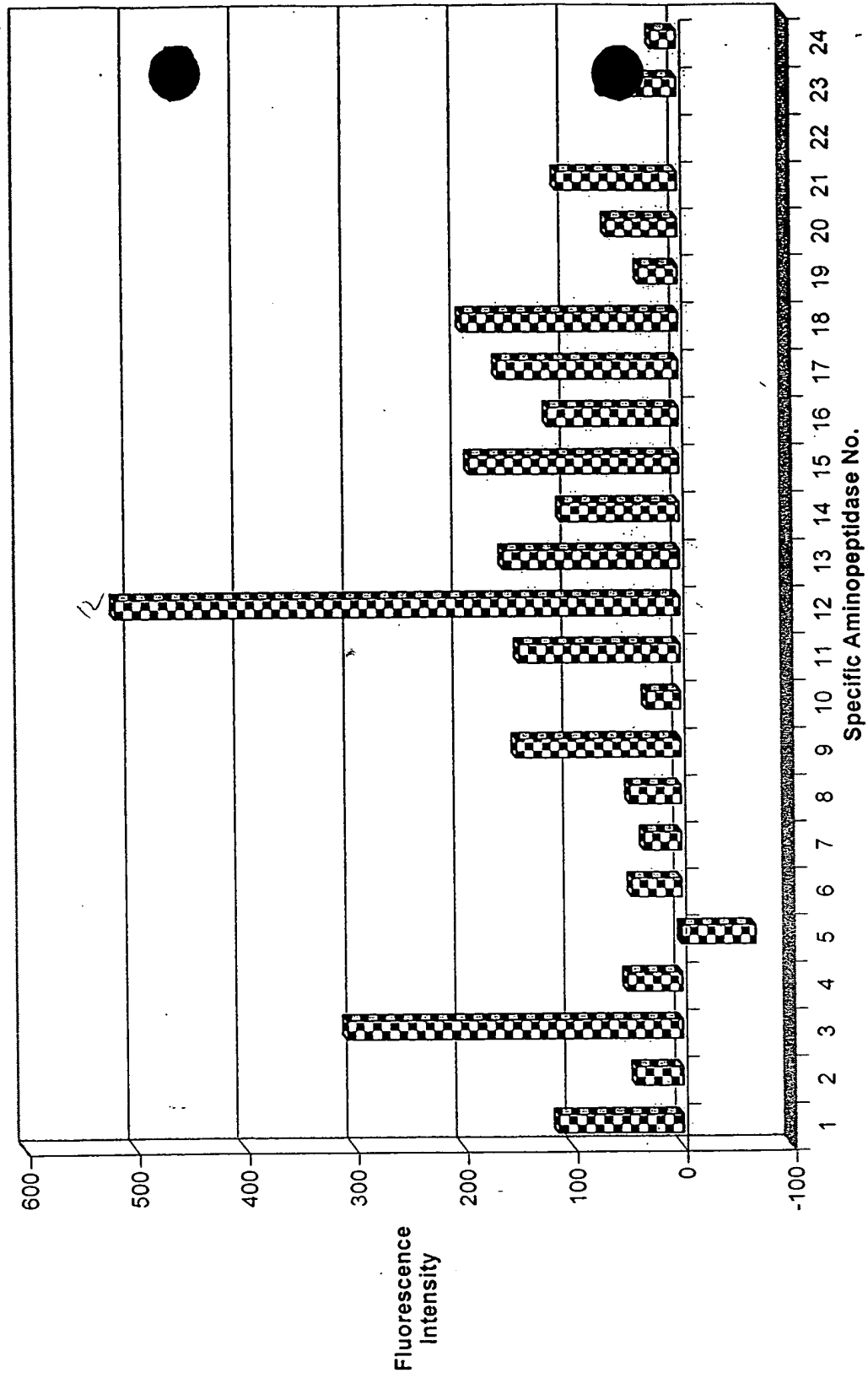

FIG. 9

Plate #2 Bacillus 1% ATCC Isolate
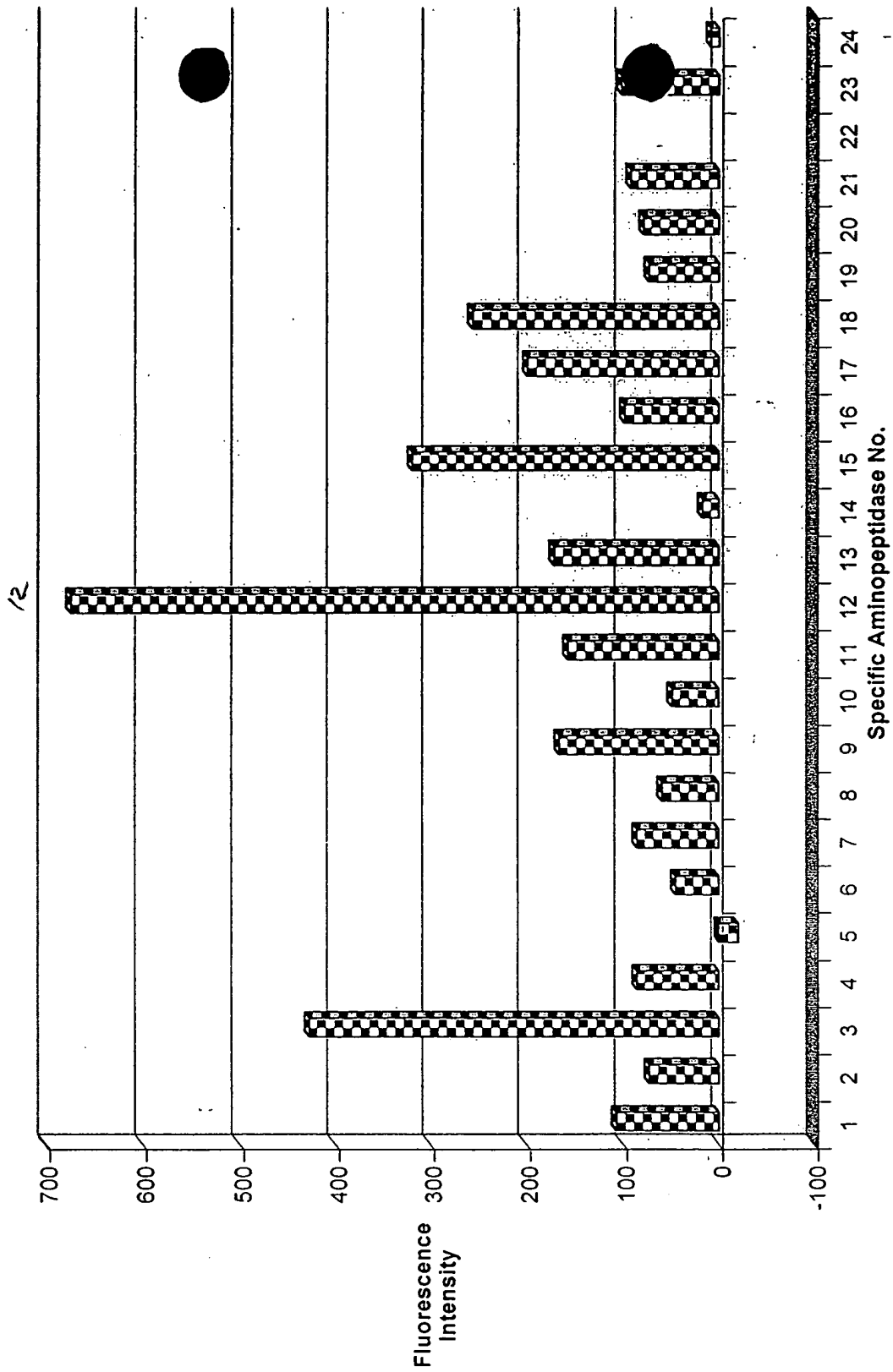

FIG. 10

Plate #3 Bacillus 30 degree Isolate

FIG. 11

Plate #4 Bacillus 20 degree Isolate

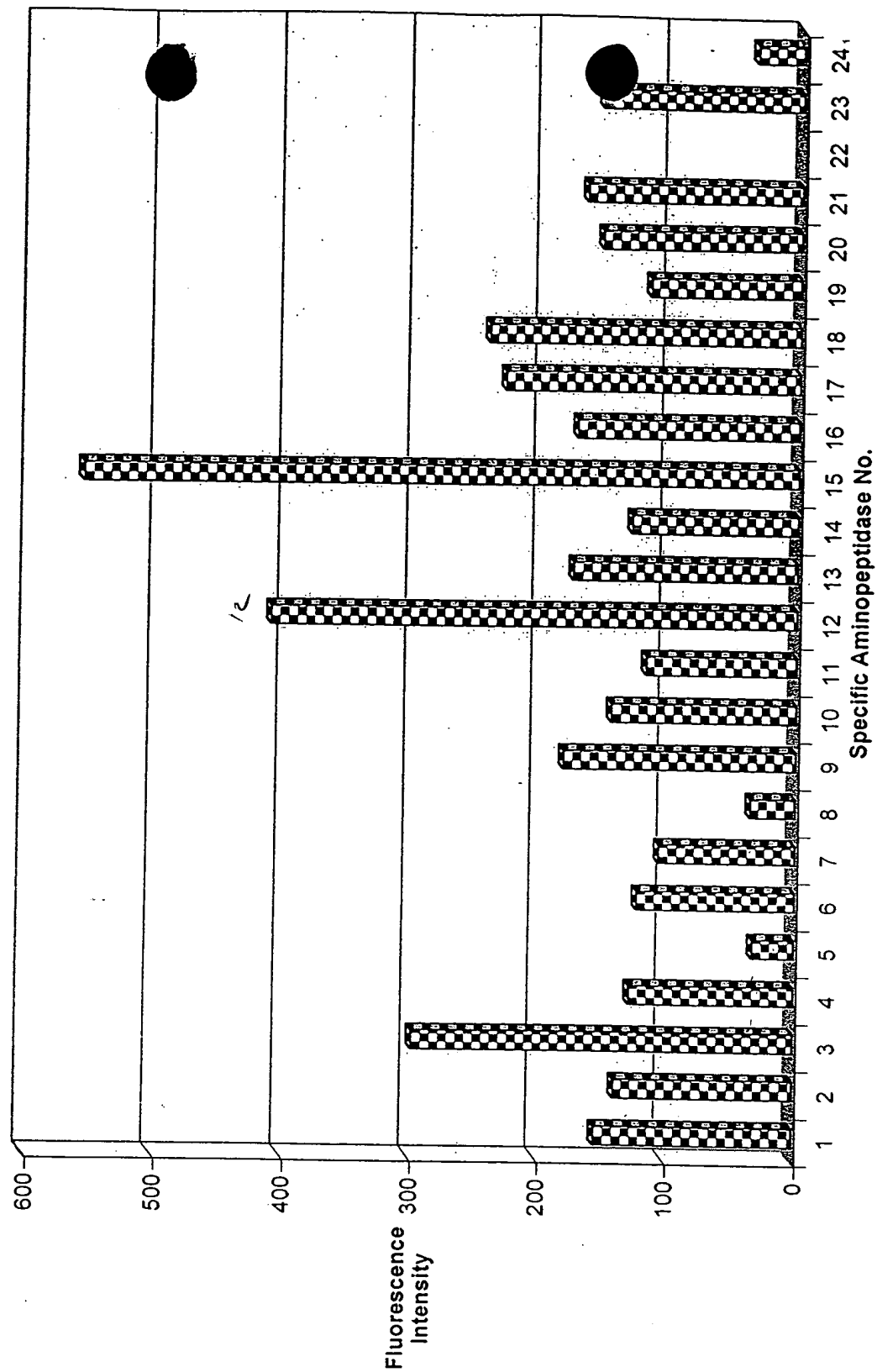Fluorescence Intensity

Specific Aminopeptidase No.

FIG. 12